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BIOTECHNOLOGY
SYSTEMS
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#9

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/901,782
Source: OIPK
Date Processed by STIC: 1/4/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE: SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission

User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/90/782

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPIIA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIEP

RAW SEQUENCE LISTING

DATE: 01/04/2002

PATENT APPLICATION: US/09/901,782

TIME: 10:19:18

Input Set : A:\09901782.txt

Output Set: N:\CRF3\01042002\I901782.raw

Does Not Comply
Corrected Diskette Needed

pp 1, 3, 5-7

3 <110> APPLICANT: VisiGen Biotechnologies
 5 <120> TITLE OF INVENTION: REAL-TIME SEQUENCE DETERMINATION
 7 <130> FILE REFERENCE: 00007/01UTL
 9 <140> CURRENT APPLICATION NUMBER: 09/901,782
 10 <141> CURRENT FILING DATE: 2001-07-09
 12 <150> PRIOR APPLICATION NUMBER: 60/ 216,594
 13 <151> PRIOR FILING DATE: 2000-07-07
 15 <160> NUMBER OF SEQ ID NOS: 48
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 38
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Synthetic DNA Sequence *see item 10 on Error Summary Sheet*
 24 <220> FEATURE:
 25 <221> NAME/KEY: promoter
 26 <222> LOCATION: (1)..(38)
 27 <223> OTHER INFORMATION: Synthetic DNA forward promoter for amplifying full-length Taq

Pol

28 I coding sequence. 5' to 3' listing
 31 <400> SEQUENCE: 1
 32 gcgaattcat gaggggggatg ctgcccctct ttgagccc 38
 35 <210> SEQ ID NO: 2
 36 <211> LENGTH: 37
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Synthetic DNA Sequence
 40 <220> FEATURE:
 41 <221> NAME/KEY: promoter
 42 <222> LOCATION: (1)..(37)
 43 <223> OTHER INFORMATION: Synthetic DNA Reverse promoter for amplifying full-length Taq

P

44 ol I coding sequence. 5' to 3' listing.
 47 <400> SEQUENCE: 2
 48 gcgaattcac cctccttgga ggagcgccag tcctccc 37
 51 <210> SEQ ID NO: 3
 52 <211> LENGTH: 37
 53 <212> TYPE: DNA
 54 <213> ORGANISM: Synthetic DNA Sequence
 56 <220> FEATURE:
 57 <221> NAME/KEY: promoter
 58 <222> LOCATION: (1)..(37)
 59 <223> OTHER INFORMATION: Synthetic DNA promoter for truncated Taq Pol I coding sequence.

60 5' to 3' listing.
 63 <400> SEQUENCE: 3
 64 aatccatggg ccctggagga ggccccctgg cccccgc 37
 67 <210> SEQ ID NO: 4
 68 <211> LENGTH: 32
 69 <212> TYPE: DNA

70 <213> ORGANISM: *Thermus aquaticus*
72 <220> FEATURE:

RAW SEQUENCE LISTING

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Input Set : A:\09901782.txt

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```

73 <221> NAME/KEY: mutation
74 <222> LOCATION: (14)..(16)
75 <223> OTHER INFORMATION: Site 643 of Taq Pol I: Alanine codon, gcc, to cysteine cysteine codon,
tgc:
76      5' to 3' listing
79 <400> SEQUENCE: 4
80 ccacacggag acctgcagct ggatgttcgg cg                      32
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 32
85 <212> TYPE: DNA
86 <213> ORGANISM: Thermus aquaticus
88 <220> FEATURE:
89 <221> NAME/KEY: Mutation
90 <222> LOCATION: (17)..(19)
91 <223> OTHER INFORMATION: Site 643 of complement strand of Taq Pol I: alanine antisense
cod
92      on, ggc, to cysteine antisense codon, gca. 5' to 3' listing.
95 <400> SEQUENCE: 5
96 cgccgaacat ccacgagcag gtctccgtgt gg                      32
99 <210> SEQ ID NO: 6
100 <211> LENGTH: 35
101 <212> TYPE: DNA
102 <213> ORGANISM: Thermus aquaticus
104 <220> FEATURE:
105 <221> NAME/KEY: Mutation
106 <222> LOCATION: (15)..(17)
107 <223> OTHER INFORMATION: Mutant Taq Pol 1: site 647 phe to cys codon mutation: ttc ->
tgc.
108      5' to 3' listing
111 <400> SEQUENCE: 6
112 ccgccagctg gatgtgcggc gtcócccggg aggcc                  35
115 <210> SEQ ID NO: 7
116 <211> LENGTH: 35
117 <212> TYPE: DNA
118 <213> ORGANISM: Thermus aquaticus
120 <220> FEATURE:
121 <221> NAME/KEY: Mutation
122 <222> LOCATION: (19)..(21)
123 <223> OTHER INFORMATION: Taq Pol I Compliment Strand: Site 647 phe to cys mutation:
gaa ->
124      gca. 5' to 3' listing.
127 <400> SEQUENCE: 7
128 ggccctcccgg gggaacggcg acatccacgt ggcgg                  35
131 <210> SEQ ID NO: 8
132 <211> LENGTH: 37
133 <212> TYPE: DNA
134 <213> ORGANISM: Thermus aquaticus
136 <220> FEATURE:
137 <221> NAME/KEY: Mutation
138 <222> LOCATION: (19)..(21)
139 <223> OTHER INFORMATION: Taq Pol I Mutation: Site 649 val to cys: gtc -> tgc. 5' to
3' lis
140      ting.

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143 <400> SEQUENCE: 8

RAW SEQUENCE LISTING

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144 gccagctgga tggtcggtg cccccgggag gccgtgg          37
147 <210> SEQ ID NO: 9
148 <211> LENGTH: 37
149 <212> TYPE: DNA
150 <213> ORGANISM: Thermus aquaticus
152 <220> FEATURE:
153 <221> NAME/KEY: Mutation
154 <222> LOCATION: (17)..(19)
155 <223> OTHER INFORMATION: Taq Pol I Mutation complementary strand: Site 649 val to
cys: gac
156      -> gca. 5' to 3' listing.
159 <400> SEQUENCE: 9
160 ccacggcctc ccggggggcag ccgaacatcc agctggc          37
163 <210> SEQ ID NO: 10
164 <211> LENGTH: 36
165 <212> TYPE: DNA
166 <213> ORGANISM: Thermus aquaticus
168 <220> FEATURE:
169 <221> NAME/KEY: Mutation
170 <222> LOCATION: (13)..(15)
171 <223> OTHER INFORMATION: Taq Pol I Mutation: Site 652 glu to cys: Codon 652 gtc ->
tgc. 5
172      ' to 3' listing.
175 <400> SEQUENCE: 10
176 ggcgtccccc ggtgcgcgt ggaccccctg atgcgc          36
179 <210> SEQ ID NO: 11
180 <211> LENGTH: 36
181 <212> TYPE: DNA
182 <213> ORGANISM: Thermus aquaticus
184 <220> FEATURE:
185 <221> NAME/KEY: Mutation
186 <222> LOCATION: (22)..(24)
187 <223> OTHER INFORMATION: Taq Pol I Mutation Complementary Strand: AA Site 652 glu to
cys:
188      antisense codon: ctc -> gca. 5' to 3' listing.
191 <400> SEQUENCE: 11
192 gcgcatcagg ggtccacgg cgcaccgggg gacgcc          36
195 <210> SEQ ID NO: 12
196 <211> LENGTH: 36
197 <212> TYPE: DNA
198 <213> ORGANISM: Thermus aquaticus
200 <220> FEATURE:
201 <221> NAME/KEY: Mutation
202 <222> LOCATION: (16)..(18)
203 <223> OTHER INFORMATION: Taq Pol I Mutation: AA Site 653 ala to cys: codon: gcc ->
tgc. 5
204      ' to 3' listing.
207 <400> SEQUENCE: 12
208 ggcgtccccc gggagtgcgt ggaccccctg atgcgc          36
211 <210> SEQ ID NO: 13
212 <211> LENGTH: 36
213 <212> TYPE: DNA
214 <213> ORGANISM: Thermus aquaticus

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```

216 <220> FEATURE:
217 <221> NAME/KEY: Mutation
218 <222> LOCATION: (19)..(21)
219 <223> OTHER INFORMATION: Taq Pol I Mutation Complimentary Strand: AA Site 653 ala to
cys:
220     antisense codon: ggc -> gca. 5' to 3' listing.
223 <400> SEQUENCE: 13
224 gcgcacacagg ggggtccacgc actcccgggg gacgcc                      36
227 <210> SEQ ID NO: 14
228 <211> LENGTH: 33
229 <212> TYPE: DNA
230 <213> ORGANISM: Thermus aquaticus
232 <220> FEATURE:
233 <221> NAME/KEY: Mutation
234 <222> LOCATION: (16)..(18)
235 <223> OTHER INFORMATION: Taq Pol I Mutation: AA 654 val to cys: codon: gtg -> tgt. 5'
to
236     3' listing.
239 <400> SEQUENCE: 14
240 gtcccccgagg aggcctgtga cccctgatg cgc                          33
243 <210> SEQ ID NO: 15
244 <211> LENGTH: 33
245 <212> TYPE: DNA
246 <213> ORGANISM: Thermus aquaticus
248 <220> FEATURE:
249 <221> NAME/KEY: Mutation
250 <222> LOCATION: (16)..(18)
251 <223> OTHER INFORMATION: Taq Pol I Mutation Complimentary Strand: AA Site 654 val to
cys:
252     antisense codon: cac -> aca. 5' to 3' listing.
255 <400> SEQUENCE: 15
256 gcgcacacagg gggtcacagg cctcccgggg gac                          33
259 <210> SEQ ID NO: 16
260 <211> LENGTH: 33
261 <212> TYPE: DNA
262 <213> ORGANISM: Thermus aquaticus
264 <220> FEATURE:
265 <221> NAME/KEY: Mutation
266 <222> LOCATION: (16)..(18)
267 <223> OTHER INFORMATION: Taq Pol I Mutation: AA 655 asp to cys: codon: gac -> tgc
270 <400> SEQUENCE: 16
271 ccccgaggagg ccgtgtgccc cctgatgcgc cgg                          33
274 <210> SEQ ID NO: 17
275 <211> LENGTH: 33
276 <212> TYPE: DNA
277 <213> ORGANISM: Thermus aquaticus
279 <220> FEATURE:
280 <221> NAME/KEY: Mutation
281 <222> LOCATION: (16)..(18)
282 <223> OTHER INFORMATION: Taq Pol I Mutation Complimentary Strand: AA Site 655 asp to
cys:
283     antisense codon: gtc -> gca. 5' to 3' listing.
286 <400> SEQUENCE: 17

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```

287 ccggcgcatc aggggggcaca cggcctcccg ggg                      33
290 <210> SEQ ID NO: 18
291 <211> LENGTH: 33
292 <212> TYPE: DNA
293 <213> ORGANISM: Thermus aquaticus
295 <220> FEATURE:
296 <221> NAME/KEY: Mutation
297 <222> LOCATION: (16)..(18)
298 <223> OTHER INFORMATION: Taq Pol I Mutation: AA 656 pro to cys: codon: ccc -> tgc. 5'
to 3
299      ' listing.
302 <400> SEQUENCE: 18
303 cgggaggccg tggactgcct gatgcgcccg gcg                      33
306 <210> SEQ ID NO: 19
307 <211> LENGTH: 33
308 <212> TYPE: DNA
309 <213> ORGANISM: Thermus aquaticus
311 <220> FEATURE:
312 <221> NAME/KEY: Mutation
313 <222> LOCATION: (16)..(18)
314 <223> OTHER INFORMATION: Taq Pol I Mutation Complimentary Strand: AA Site 656 pro to
cys:
315      antisense codon: ggg -> gca. 5' to 3' listing.
318 <400> SEQUENCE: 19
319 cgcccggcgc atcaggcagt ccacggcctc ccg                      33
322 <210> SEQ ID NO: 20
323 <211> LENGTH: 30
324 <212> TYPE: DNA
325 <213> ORGANISM: Thermus aquaticus
327 <220> FEATURE:
328 <221> NAME/KEY: Mutation
329 <222> LOCATION: (13)..(15)
330 <223> OTHER INFORMATION: Taq Pol I Mutation: AA 657 leu to cys: codon: ctg -> tgc. 5'
to 3
331      ' listing.
334 <400> SEQUENCE: 20
335 gccgtggacc cctgcatgcg ccgggcccgc                      30
338 <210> SEQ ID NO: 21
339 <211> LENGTH: 30
340 <212> TYPE: DNA
341 <213> ORGANISM: Thermus aquaticus
343 <220> FEATURE:
344 <221> NAME/KEY: Mutation
345 <222> LOCATION: (16)..(18)
346 <223> OTHER INFORMATION: Taq Pol I Mutation Complimentary Strand: AA Site 657 leu to
cys:
347      antisense codon: cag -> gca. 5' to 3' listing.
350 <400> SEQUENCE: 21
351 ggccgccccg cgcattgcagg ggtccacggc
354 <210> SEQ ID NO: 22
355 <211> LENGTH: 30
356 <212> TYPE: DNA
357 <213> ORGANISM: Thermus aquaticus

```

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

VERIFICATION SUMMARY

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